GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 11:15:29 ; Search time 196.545 Seconds
(without alignments)
263.532 Million cell updates/sec

Title: US-10-086-184-1
Perfect score: 23
Sequence: 1 aaatcggctccgaggcgggaaac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	65.2	40	22	AAD14572	Arabidopsis thalia
	2	15	65.2	40	22	AAS07877	Binding site selec
	3	15	65.2	40	22	AAD08945	Arabidopsis thalia
	4	15	65.2	40	22	AAS03391	A group IA abscisi
	5	15	65.2	40	22	AAS00410	ABRE binding seque
c	6	14.8	64.3	18	22	AAH47535	Human Her-3 mRNA i
c	7	14.6	63.5	31	20	AAX06374	Human biallelic po
c	8	14.2	61.7	38	21	AAC73135	Single base extens
c	9	13.8	60.0	23	20	AAX77145	Nerve mutation fac
c	10	13.8	60.0	26	17	AAT08994	Insulin response e
	11	13.8	60.0	29	18	AAT51155	Homeoprotein regul
	12	13.8	60.0	33	14	AAQ49298	Degenerin PCR prim
c	13	13.8	60.0	37	17	AAT08992	Transfection analy
	14	13.6	59.1	29	15	AAQ61760	HEV strain BUR-121
	15	13.6	59.1	29	17	AAT27471	HEV strain Burma-1
	16	13.6	59.1	29	19	AAV71681	HEV ORF proteins e
c	17	13.6	59.1	34	19	AAV40446	Primer 2, used to
c	18	13.6	59.1	34	20	AAX79944	PCR primer for EDD
	19	13.4	58.3	15	21	AAC73137	Forward primer #17
	20	13.4	58.3	18	20	AAX32002	MSH2 gene specific
	21	13.4	58.3	26	22	AAI61811	Soybean 240017 reg
c	22	13.4	58.3	33	15	AAQ44662	PCR primer for pro
c	23	13.4	58.3	33	15	AAQ44660	PCR primer for amp
	24	13.4	58.3	36	24	ABA01674	Human androgen rec
	25	13.4	58.3	40	21	AAC73139	Single base extens
c	26	13.2	57.4	24	21	AAA87589	Rat hepatocyte car
c	27	13.2	57.4	27	19	AAV23514	Primer for mouse R
	28	13.2	57.4	33	14	AAQ49299	Degenerin PCR prim
	29	13	56.5	27	18	AAX68630	Human flt1 VEGF re
	30	13	56.5	28	18	AAT66979	Human endothelial-
	31	13	56.5	28	21	AAZ87149	Human EMAP III PCR
	32	13	56.5	28	21	AAZ87151	Human EMAP III PCR
	33	12.8	55.7	23	15	AAQ66278	PCR primer for amp
c	34	12.8	55.7	23	24	ABL51612	Chimeric polymeras
	35	12.8	55.7	23	24	ABL51613	Chimeric polymeras
	36	12.8	55.7	27	22	AAF99060	Immunostimulatory
c	37	12.8	55.7	27	22	AAF99061	Immunostimulatory
	38	12.8	55.7	27	22	AAF99864	Immunostimulatory
c	39	12.8	55.7	27	24	ABL38717	Immunostimulatory
	40	12.8	55.7	27	24	ABL39012	Immunostimulatory
	41	12.8	55.7	30	14	AAQ49268	ced-4 primer. Syn
	42	12.8	55.7	30	24	ABK94879	Fat regulated gene
	43	12.6	54.8	30	22	ABA02872	Soybean coproporph
	44	12.6	54.8	30	22	AAH46574	Soybean coproporph
c	45	12.6	54.8	30	23	ABI97714	Endogenous human G

ALIGNMENTS

RESULT 1
AAD14572
ID AAD14572 standard; DNA; 40 BP.
XX
AC AAD14572;
XX
DT 01-NOV-2001 (first entry)
XX
DE Arabidopsis thaliana ABF binding sequence #19.
XX
KW Abscisic acid responsive element; ABRE; ABRE-binding factor; ABF;
KW stress treatment; transgenic plant; environmental stress; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT misc_feature 19..29
FT /*tag= a
FT /note= "Conserved region"
FT misc_feature 29
FT /*tag= b
FT /note= "S is present at this location in the
FT sequence shown in column 43 of the specification"
XX
PN US6232461-B1.
XX
PD 15-MAY-2001.
XX
PF 19-SEP-2000; 2000US-0665309.
XX
PR 12-OCT-1999; 99US-0416050.
XX

```
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-366358/38.
XX
PT   New nucleic acid encoding abscisic acid responsive element binding
PT   factor 4, useful for generating transgenic plants, which are tolerant
PT   to multiple environmental stresses -
XX
PS   Disclosure; Fig 5B; 42pp; English.
XX
CC   The invention relates to nucleic acid encoding the Abscisic acid
CC   responsive element (ABRE)-binding factor 4 (ABF4). ABF4 belongs to
CC   the ABF family of factors which bind abscisic acid responsive elements
CC   in plants. Expression of ABFs is inducible by abscisic acid and various
CC   stress treatments. ABFs have the potential to activate a large number
CC   of abscisic acid/stress responsive genes and thus a nucleic acid
CC   molecule encoding ABF4 is useful for generating transgenic plants
CC   that are tolerant to multiple environmental stresses. The present
CC   sequence is Arabidopsis thaliana ABF binding sequence which contains
CC   the group IA consensus sequence.
XX
SQ   Sequence 40 BP; 9 A; 12 C; 12 G; 7 T; 0 other;

  Query Match             65.2%;  Score 15;  DB 22;  Length 40;
  Best Local Similarity   78.3%;  Pred. No. 8e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 AAATCGGCTCCGAGGCGGGAAAC 23
           || ||| |||  |||||||| ||
Db       2 AATTCGCCTCTAAGGCGGGACAC 24


RESULT 2
AAS07877
ID   AAS07877 standard; DNA; 40 BP.
XX
AC   AAS07877;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Binding site selection assay group IA sequence #19.
XX
KW   Abscisic acid responsive element binding factor; ABF; bZIP; ss; G/ABRE;
KW   G-box-like ABRE; coupling element-like ABRE; C/ABRE; transgenic plant;
KW   stress responsive gene; environmental stress; cress;
KW   binding site selection assay.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    20..29
FT                   /*tag=  a
FT                   /note= "Group IA consensus sequence"
XX
PN   EP1097999-A2.
XX
PD   09-MAY-2001.
XX
PF   29-JUN-2000; 2000EP-0305459.
XX
PR   04-NOV-1999;   99KR-0048477.
XX
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-337113/36.
XX
PT   Nucleic acid encoding novel transcription factors that bind to various
PT   abscisic acid responsive elements, for generating stress tolerant
PT   transgenic plants  -
XX
PS   Disclosure; Fig 5B; 37pp; English.
XX
CC   The sequence represents an oligonucleotide studied in a binding site
CC   selection assay, for studying abscisic acid responsive element binding
CC   factor (ABF) proteins. The oligonucleotide contains the IA consensus
CC   sequence. ABFs are bZIP class transcription factors that can bind to two
CC   classes of ABRE, namely G-box-like ABREs (G/ABRE) and coupling
CC   element-like ABREs (C/ABRE). Expression of ABF is inducible by abscisic
CC   acid and various stress treatments and they can transactivate an
CC   ABRE-containing reporter gene in yeast. Therefore, the ABFs are useful
CC   for activating a large number of abscisic acid or stress responsive genes
CC   and for generating transgenic plants that are tolerant to multiple
CC   environmental stresses.
XX
SQ   Sequence 40 BP; 9 A; 12 C; 12 G; 7 T; 0 other;

  Query Match             65.2%;  Score 15;  DB 22;  Length 40;
  Best Local Similarity   78.3%;  Pred. No. 8e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 AAATCGGCTCCGAGGCGGGAAAC 23
           || ||| |||  |||||||| ||
Db       2 AATTCGCCTCTAAGGCGGGACAC 24


RESULT 3
AAD08945
ID   AAD08945 standard; DNA; 40 BP.
XX
AC   AAD08945;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Arabidopsis thaliana ABF binding sequence #18.
XX
KW   Abscisic acid responsive element binding factor; ABF; ABRE;
KW   bZIP class transcription factor; transgenic plant; ds.
XX
OS   Arabidopsis thaliana.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    19..29
FT                   /*tag=  a
FT                   /note= "Conserved region"
FT   misc_feature    29
FT                   /*tag=  b
FT                   /note= "Base "S" is found at this location in the
FT                   sequence shown as SEQ ID NO: 51 in the sequence listing"
XX
PN   US6245905-B1.
XX
PD   12-JUN-2001.
XX
PF   14-SEP-2000; 2000US-0661569.
XX
PR   12-OCT-1999;   99US-0416050.
XX
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-380516/40.
XX
PT   New abscisic acid responsive element binding factor 2 useful for
PT   activating abscisic acid/stress responsive genes, and generating
PT   transgenic plants that are tolerant to multiple environmental stresses
PT   -
XX
PS   Disclosure; Fig 5B; 42pp; English.
XX
CC   The patent discloses novel abscisic acid (ABA) responsive element
CC   (ABRE) binding factors (ABFs). ABFs are basic leucine zipper (bZIP)
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CC   class transcription factors that bind to both G-box-like ABREs (G/ABREs)
CC   and coupling element like ABREs (C/ABREs). ABFs have the potential to
CC   activate a large number of abscisic acid/stress responsive genes, and
CC   are therefore used to generate transgenic plants that are tolerant to
CC   multiple environmental stresses.
CC   The present DNA sequence is Arabidopsis thaliana ABF binding sequence
CC   which contains the group IA consensus sequence.
CC   Note: This sequence is stated to be the same as that shown as
CC   SEQ ID NO: 51 in the sequence listing of the specification. However
CC   the sequences differ at position 29.
XX
SQ   Sequence 40 BP; 9 A; 12 C; 12 G; 7 T; 0 other;

  Query Match             65.2%;  Score 15;  DB 22;  Length 40;
  Best Local Similarity   78.3%;  Pred. No. 8e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AAATCGGCTCCGAGGCGGGAAAC 23
          || ||| |||  |||||||| ||
Db      2 AATTCGCCTCTAAGGCGGGACAC 24


RESULT 4
AAS03391
ID   AAS03391 standard; DNA; 40 BP.
XX
AC   AAS03391;
XX
DT   29-AUG-2001  (first entry)
XX
DE   A group IA abscisic acid response element (G/ABRE).
XX
KW   Abscisic acid response element; G/ABRE; ABRE binding factor; ABF;
KW   transgenic plant; stress responsive gene; environmental stress response;
KW   probe; ds; G-box.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   protein_bind    19..27
FT                   /*tag=  a
FT                   /bound_moiety= "ABF"
XX
PN   US6218527-B1.
XX
PD   17-APR-2001.
XX
PF   19-SEP-2000; 2000US-0664800.
XX
PR   12-OCT-1999;   99US-0416050.
XX
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-281059/29.
XX
PT   Isolated nucleic acid molecule for generating environmental-stress
PT   tolerant transgenic plants, encodes abscisic acid responsive
PT   element-binding factor 3 -
XX
PS   Disclosure; Column 43; 43pp; English.
XX
CC   The sequence represents a group IA G-box containing abscisic acid
CC   response element (G/ABRE), used in a gel mobility shift assay, testing
CC   for the binding of ABRE binding factor, ABF1. The nucleic acid encoding
CC   an ABF can be used to generate transgenic plants that are tolerant to
CC   multiple environmental stresses e.g. drought, high salt, and cold/
CC   freezing. Expression of the binding factor is inducible by abscisic acid
CC   and various stress treatments, and can transactivate an abscisic acid
CC   responsive element (ABRE)-containing a reporter gene in yeast. The
CC   binding factor can activate a number of abscisic acid/stress responsive
CC   genes.
XX
SQ   Sequence 40 BP; 9 A; 11 C; 12 G; 7 T; 1 other;

  Query Match             65.2%;  Score 15;  DB 22;  Length 40;
  Best Local Similarity   78.3%;  Pred. No. 8e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AAATCGGCTCCGAGGCGGGAAAC 23
          || ||| |||  |||||||| ||
Db      2 AATTCGCCTCTAAGGCGGGACAC 24


RESULT 5
AAS00410
ID   AAS00410 standard; cDNA; 40 BP.
XX
AC   AAS00410;
XX
DT   25-MAY-2001  (first entry)
XX
DE   ABRE binding sequence 45, identified from binding site selection.
XX
KW   Abscisic acid responsive element binding factor 1; ABF1; plant hormone;
KW   drought; ABA-responsive element; ABRE; ABRE-binding factor; ABF;
KW   basic leucine zipper; bZIP; G/ABRE; C/ABRE; transgenic plant;
KW   environmental stress; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6194559-B1.
XX
PD   27-FEB-2001.
XX
PF   12-OCT-1999;   99US-0416050.
XX
PR   12-OCT-1999;   99US-0416050.
XX
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-217937/22.
XX
PT   New nucleic acid molecule encoding Abscisic acid responsive element
PT   binding factor 1 (ABF1) which can be used to generate transgenic plants
PT   that are tolerant to multiple environmental stresses -
XX
PS   Disclosure; Fig 5B; 42pp; English.
XX
CC   The sequence represents the ABRE binding sequence 45, identified from
CC   binding site selection analysis of abscisic acid responsive element
CC   binding factors (ABFs), isolated from an Arabidopsis cDNA library.
CC   Abscisic acid (ABA) is a major plant hormone involved in response to
CC   adverse environmental conditions such as drought, high salt and cold/
CC   freezing. This response involves induced expression of various genes.
CC   ABA-responsive elements (ABREs) are cis-regulatory elements that mediate
CC   the ABA-modulated gene expression, and interact with a novel class of
CC   ABRE-binding factors (ABFs). ABFs are basic leucine zipper (bZIP) class
CC   transcription factors that bind to both G/ABREs and C/ABREs. ABFs have
CC   the potential to activate a large number of ABA/stress responsive genes
CC   and can be used to generate transgenic plants that are tolerant to
CC   multiple environmental stresses.
XX
SQ   Sequence 40 BP; 9 A; 11 C; 12 G; 7 T; 1 other;

  Query Match             65.2%;  Score 15;  DB 22;  Length 40;
  Best Local Similarity   78.3%;  Pred. No. 8e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 AAATCGGCTCCGAGGCGGGAAAC 23
          || ||| |||  |||||||| ||
Db      2 AATTCGCCTCTAAGGCGGGACAC 24
```

RESULT 6
AAH47535/c
ID AAH47535 standard; DNA; 18 BP.
XX
AC AAH47535;
XX
DT 30-NOV-2001 (first entry)
XX
DE Human Her-3 mRNA inhibiting antisense oligo ISIS # 19550.
XX
KW Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
KW antiinflammatory; cytostatic; antibacterial; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US6277640-B1.
XX
PD 21-AUG-2001.
XX
PF 31-JUL-2000; 2000US-0630706.
XX
PR 31-JUL-2000; 2000US-0630706.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM;
XX
DR WPI; 2001-535134/59.
XX
PT Antisense compounds capable of modulating expression of human Her-3,
PT member of epidermal growth factor family of receptor/tyrosine kinases,
PT useful for preventing or delaying infection, inflammation or tumor
PT formation -
XX
PS Claim 1; Column 42; 49pp; English.
XX
CC The invention provides antisense compounds capable of inhibiting the
CC expression of human Her-3, a member of epidermal growth factor (EGF)
CC family of receptor/tyrosine kinases. The antisense oligonucleotides are
CC useful for inhibiting the expression of Her-3 in cells or tissues. They
CC are commonly used as research reagents and in diagnostics for example, to
CC elucidate the function of particular genes. The antisense compounds are
CC also useful for distinguishing between functions of various members of a
CC biological pathway and for research use. They are also utilized for
CC diagnostics, therapeutics, prophylaxis and in kits. They are useful
CC prophylactically, e.g. to prevent or delay infection, inflammation or
CC tumor formation. Sequences AAH47532-47615 represent chimeric antisense
CC phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,
CC used for the inhibition of Her-3 mRNA expression.
XX
SQ Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 other;

Query Match 64.3%; Score 14.8; DB 22; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GGCTCCGAGGCGGGAAAC 23
||||||||||| ||| |||
Db 18 GGCTCCGAGGTGGGCAAC 1

RESULT 7
AAX06374/c
ID AAX06374 standard; DNA; 31 BP.
XX
AC AAX06374;
XX
DT 31-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic DNA fragment SGC33319.
XX
KW Polymorphism; biallelic; paternity testing; forensic; genetic mapping;
KW phenotypic typing; medicament; disease; marker; human; ss.
XX
OS Homo sapiens.
XX
PN WO9858529-A2.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-US12930.
XX
PR 24-JUN-1997; 97US-0050594.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Berno A, Chee M, Fan J, Lipshutz RJ;
XX
DR WPI; 1999-080963/07.
XX
PT New nucleic acid segments containing polymorphic sites - used for,
PT e.g. detecting a disease phenotype, in forensics, paternity testing
PT or genetic mapping of phenotypic traits
XX
PS Claim 1; Page 23; 61pp; English.
XX
CC Sequences AAX06101-X06558 represent human DNA fragments which contain
CC biallelic polymorphic markers. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These
CC fragments can be used in a method for determining polymorphic forms in
CC an individual. The invention further provides computer-readable storage
CC medium for storing data for access by an application programme being
CC executed on a data processing system. Such a method comprises a data
CC structure stored in the computer-readable storage medium, the data
CC structure including information resident in a database used by the
CC application programme and including records, each record comprising
CC information identifying a polymorphism shown in the above sequences. The
CC products and methods can be used for analysing polymorphic sites in
CC individuals for testing for the presence of a disease phenotype or in
CC forensics, paternity testing or genetic mapping of phenotypic traits.
CC They can also be used for the production of polypeptides expressed by
CC variant genes and for the production of transgenic animals. The nucleic
CC acid segments can also be used in the manufacture of medicaments for the
CC treatment or prophylaxis of diseases.
XX
SQ Sequence 31 BP; 5 A; 8 C; 8 G; 9 T; 1 other;

Query Match 63.5%; Score 14.6; DB 20; Length 31;
Best Local Similarity 73.9%; Pred. No. 1.2e+03;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AAATCGGCTCCGAGGCGGGAAAC 23
| ||| ||| |||| :| |||| |
Db 30 ACATCAGCTACGAGKCTGGAATC 8

RESULT 8
AAC73135/c
ID AAC73135 standard; DNA; 38 BP.
XX
AC AAC73135;
XX
DT 02-FEB-2001 (first entry)
XX
DE Single base extension primer #16 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.

```
XX
PF   27-MAR-2000; 2000WO-US08069.
XX
PR   26-MAR-1999;   99US-0126473.
PR   23-JUN-1999;   99US-0140359.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Fan J,  Hirschhorn JN,  Huang X,  Kaplan P,  Lander ES,  Lockhart DJ;
PI   Ryder T,  Sklar P;
XX
DR   WPI; 2000-656171/63.
XX
PT   Universal array of oligonucleotides tags attached to a solid substrate
PT   along with locus-specific tagged oligonucleotides useful in genotyping
PT   using single base extension reactions  -
XX
PS   Example 7; Page 49; 83pp; English.
XX
CC   The present invention relates to an oligonucleotide array comprising
CC   oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC   array is useful for genotyping a nucleic acid sample at one or more loci
CC   via single base extension (SBE) reactions. A pair of primers is used to
CC   amplify a polymorphic locus in a sample e.g. a single nucleotide
CC   polymorphism (SNP). The amplified nucleic acid product is then used as a
CC   template in a SBE reaction with an extension primer. The present sequence
CC   is one such SBE reaction primer used in the method of the present
CC   invention. The SBE reaction products are used to form the oligonucleotide
CC   array.
XX
SQ   Sequence 38 BP; 7 A; 13 C; 10 G; 8 T; 0 other;

  Query Match             61.7%;  Score 14.2;  DB 21;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 TCGGCTCCGAGGCGGGAAA 22
           ||||||||||| || | |
Db      36 TCGGCTCCGAGGTGGAAGA 18


RESULT 9
AAX77145/c
ID   AAX77145 standard; DNA; 23 BP.
XX
AC   AAX77145;
XX
DT   03-AUG-1999  (first entry)
XX
DE   Nerve mutation factor DNA amplifying primer.
XX
KW   Nerve mutation factor; chromosome 10; glioma; tumour suppressor;
KW   brain tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9925827-A1.
XX
PD   27-MAY-1999.
XX
PF   24-AUG-1998;   98WO-JP03737.
XX
PR   14-NOV-1997;   97JP-0313211.
XX
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI   Nakamura H,  Nakata M,  Saya H,  Yoshida M;
XX
DR   WPI; 1999-347474/29.
XX
PT   Human gene on chromosome 10 homologous to Drosophila neuralized
PT   gene, useful in the diagnosis and gene therapy of brain tumors
XX
PS   Examples; Page 24; 78pp; Japanese.
XX
CC   The invention relates to a  protein which is a nerve mutation factor and
CC   is the expression product of a gene located on chromosome 10. The gene
CC   is in a region frequently deleted in highly malignant gliomas. Sequences
CC   (AAX77135 and AAX77136) encoding human and mouse nerve mutation factors
CC   (AAY21558 and AAY21559) are provided. The protein is believed to have
CC   tumour suppressor activity. Polynucleotide sequences and antibodies to
CC   the protein are diagnostic reagents for highly malignant brain tumors
CC   such as astrocytoma where chromosome 10 deletion commonly occurs. The
CC   gene may also be used for gene therapy of such tumours.
XX
SQ   Sequence 23 BP; 2 A; 8 C; 8 G; 5 T; 0 other;

  Query Match             60.0%;  Score 13.8;  DB 20;  Length 23;
  Best Local Similarity   88.2%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 AAATCGGCTCCGAGGCG 17
             ||| ||||| |||||||
Db      22 AAAGCGGCTGCGAGGCG 6


RESULT 10
AAT08994/c
ID   AAT08994 standard; DNA; 26 BP.
XX
AC   AAT08994;
XX
DT   25-JUL-1996  (first entry)
XX
DE   Insulin response element A minimal DNA binding element.
XX
KW   Insulin response element A; IRE-A; E2F; liver IRP-A;
KW   Rb-associated protein; RBAP-1; E2F-1; rapamycin; inhibition;
KW   insulin-induced; expression; carbohydrate uptake;
KW   triglyceride biosynthesis; treatment; prevention; obesity;
KW   type II diabetes mellitus; insulin dependent tumours;
KW   minimal DNA binding element; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..17
FT                   /*tag=  a
FT                   /note= "contact sequence"
FT   misc_feature    1
FT                   /*tag=  b
FT                   /note= "contact point"
FT   misc_feature    5
FT                   /*tag=  c
FT                   /note= "contact point"
FT   misc_feature    6
FT                   /*tag=  d
FT                   /note= "contact point"
FT   misc_feature    7
FT                   /*tag=  e
FT                   /note= "contact point"
FT   misc_feature    9
FT                   /*tag=  f
FT                   /note= "contact point"
FT   misc_feature    10
FT                   /*tag=  g
FT                   /note= "contact point"
FT   misc_feature    12
FT                   /*tag=  h
FT                   /note= "contact point"
FT   misc_feature    14
FT                   /*tag=  i
FT                   /note= "contact point"
FT   misc_feature    17
FT                   /*tag=  j
```

```
FT                   /note= "contact point"
XX
PN   WO9531104-A1.
XX
PD   23-NOV-1995.
XX
PF   10-MAY-1995;   95WO-US05835.
XX
PR   13-MAY-1994;   94US-0242409.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Alexander-Bridges MC,  Zhao H;
XX
DR   WPI; 1996-049292/05.
XX
PT   Use of rapamycin to inhibit insulin-induced adiposis - for treating
PT   insulin-induced obesity, weight gain and other conditions associated
PT   with hyperinsulinaemia
XX
PS   Example; Page 27; 55pp; English.
XX
CC   The present sequence is the insulin response element A (IRE-A)
CC   minimal DNA binding element, which binds, with identical contact
CC   sequence contact points, to liver IRP-A, and the cloned
CC   Rb-associated protein RBAP-1 (E2F-1). This information was used in
CC   the development of the invention, i.e. rapamycin inhibition of
CC   insulin-induced expression of carbohydrate uptake, and
CC   triglyceride biosynthesis genes, useful in the treatment and
CC   prevention of obesity, type II diabetes mellitus and insulin
CC   dependent tumours, etc..
XX
SQ   Sequence 26 BP; 4 A; 10 C; 4 G; 8 T; 0 other;

  Query Match             60.0%;  Score 13.8;  DB 17;  Length 26;
  Best Local Similarity   88.2%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       6 GGCTCCGAGGCGGGAAA 22
           ||||  ||||||||||
Db      18 GGCTGAGAGGCGGGAAA 2


RESULT 11
AAT51155
ID   AAT51155 standard; DNA; 29 BP.
XX
AC   AAT51155;
XX
DT   18-AUG-1997  (first entry)
XX
DE   Homeoprotein regulator of insulin gene expression primer GST-GGGS.
XX
KW   Antibody; diabetes; breast cancer; insulin dependent diabetes;
KW   hypoglycaemia; hyperglycaemia; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9636711-A2.
XX
PD   21-NOV-1996.
XX
PF   09-MAY-1996;   96WO-US06608.
XX
PR   09-MAY-1995;   95US-0437607.
XX
PA   (SALK ) SALK INST.
PA   (STRA-) STRANG CANCER PREVENTION CENT.
XX
PI   Leonard JN,  Montminy MR;
XX
DR   WPI; 1997-012086/01.
XX
PT   New homeo:protein regulator of insulin gene expression - and related
PT   DNA and antibodies, useful for detecting e.g diabetes or breast
PT   cancer
XX
PS   Examples; Page 44; 96pp; English.
XX
CC   The present sequence is primer GST-GGGS used in the examples in order
CC   to more fully illustrate the preferred embodiments of the invention.
CC   The HoxB13 gene encodes a homeoprotein regulator of insulin gene
CC   expression. The novel homeoprotein regulator of insulin gene expression
CC   is a protein (or its active fragments, agonists and/or mimics) which
CC   binds the FLAT element of an insulin gene promoter; which is modulated
CC   by a Ca2+-dependent CaM kinase IV; and which is homologous to a sequence
CC   encoded by a Hox gene complex. Detection of altered levels of the HoxB13
CC   protein indicates a disease related to glucose homeostasis, particularly
CC   (non-)insulin dependent diabetes, hypo- or hyper-glycaemia, or also
CC   breast cancer. Antibodies are useful as reagents for immunoassays. The
CC   protein and compounds that promote and inhibit its production or
CC   activity or its specific binding partners, are useful for preventing or
CC   treating the specified diseases, especially where insulin is also being
CC   administrated.
XX
SQ   Sequence 29 BP; 4 A; 9 C; 10 G; 6 T; 0 other;

  Query Match             60.0%;  Score 13.8;  DB 18;  Length 29;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 CGGCTCCGAGGCGGGAA 21
           ||| ||||||||||| |
Db       3 CGGATCCGAGGCGGGTA 19


RESULT 12
AAQ49298
ID   AAQ49298 standard; DNA; 33 BP.
XX
AC   AAQ49298;
XX
DT   28-APR-1994  (first entry)
XX
DE   Degenerin PCR primer.
XX
KW   Long-distance homology; evolution; nematode;
KW   hybridisation; lower organism; structural homologue;
KW   Alzheimer's disease; cell death gene; PCR; polymerase chain reaction;
KW   ciona intestinalis; echinoderm; lamprey; puffer fish;
KW   mammal; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9320237-A.
XX
PD   14-OCT-1993.
XX
PF   01-APR-1993;   93WO-US03102.
XX
PR   01-APR-1992;   92US-0861458.
XX
PA   (CAMB-) CAMBRIDGE NEUROSCIENCE INC.
XX
PI   Johnson CD,  Marchionni MA;
XX
DR   WPI; 1993-336943/42.
XX
PT   Long-distance homology cloning of genes from lower organisms -
PT   used to identify DNA that codes for evolutionary conserved
PT   aminoacid sequences
XX
PS   Disclosure; Fig 14; 188pp; English.
XX
CC   The primers (AAQ49297-Q49348) and probes (AAQ49322-Q49348) are used to
CC   isolate degenerin homologues from genomic DNA templates from three
```

```
CC   nematodes: Caenorhabditis elegans, C. briggsae, Ascaris suum.
CC   The primers were based on area I and II amino acid sequences common
CC   to the degenerin gene family members DEG-1 and MEC-4 from C. elegans.
XX
SQ   Sequence 33 BP; 6 A; 7 C; 9 G; 5 T; 6 other;

  Query Match             60.0%;  Score 13.8;  DB 14;  Length 33;
  Best Local Similarity   65.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 AAATCGGCTCCGAGGCGGGAAAC 23
           || |||| ||||    | ||:||:
Db       3 AATTCGGATCCGGNACNGGRAAY 25


RESULT 13
AAT08992/c
ID   AAT08992 standard; DNA; 37 BP.
XX
AC   AAT08992;
XX
DT   25-JUL-1996  (first entry)
XX
DE   Transfection analysis minimal binding motif.
XX
KW   Insulin response element A; IRE-A; E2F; liver IRP-A;
KW   Rb-associated protein; RBAP-1; E2F-1; rapamycin; inhibition;
KW   insulin-induced; expression; carbohydrate uptake;
KW   triglyceride biosynthesis; treatment; prevention; obesity;
KW   type II diabetes mellitus; insulin dependent tumours;
KW   electrophoretic mobility shift assay; EMSA;
KW   transfection analysis; minimal binding motif; ss.
XX
OS   Synthetic.
XX
PN   WO9531104-A1.
XX
PD   23-NOV-1995.
XX
PF   10-MAY-1995;   95WO-US05835.
XX
PR   13-MAY-1994;   94US-0242409.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Alexander-Bridges MC,  Zhao H;
XX
DR   WPI; 1996-049292/05.
XX
PT   Use of rapamycin to inhibit insulin-induced adiposis - for treating
PT   insulin-induced obesity, weight gain and other conditions associated
PT   with hyperinsulinaemia
XX
PS   Example; Page 21; 55pp; English.
XX
CC   The present sequence is a transfection analysis minimal binding
CC   motif, which was used in an electrophoretic mobility shift assay to
CC   characterise insulin response element A (IRE-A) like and E2F like
CC   binding activities. IRE-A normally binds, with identical contact
CC   sequence contact points, to liver IRP-A, and the cloned
CC   Rb-associated protein RBAP-1 (E2F-1). This information was used in
CC   the development of the invention, i.e. rapamycin inhibition of
CC   insulin-induced expression of carbohydrate uptake, and
CC   triglyceride biosynthesis genes, useful in the treatment and
CC   prevention of obesity, type II diabetes mellitus and insulin
CC   dependent tumours, etc..
XX
SQ   Sequence 37 BP; 8 A; 14 C; 5 G; 10 T; 0 other;

  Query Match             60.0%;  Score 13.8;  DB 17;  Length 37;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       6 GGCTCCGAGGCGGGAAA 22
           ||||  ||||||||||
Db      29 GGCTGAGAGGCGGGAAA 13


RESULT 14
AAQ61760
ID   AAQ61760 standard; cDNA; 29 BP.
XX
AC   AAQ61760;
XX
DT   21-OCT-1994  (first entry)
XX
DE   HEV strain BUR-121 primer R81.
XX
KW   Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; PCR;
KW   antibody; detection; diagnosis; primates; stool suspension; amplify;
KW   polymerase chain reaction; primer; burma; strain BUR-121; ss.
XX
OS   Synthetic.
XX
PN   WO9406913-A.
XX
PD   31-MAR-1994.
XX
PF   17-SEP-1993;   93WO-US08849.
XX
PR   18-SEP-1992;   92US-0947263.
XX
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Emerson SU,  Purcell RH,  Tsarev SA;
XX
DR   WPI; 1994-118462/14.
XX
PT   Purified hepatitis E strain SAR-55 virus - used to develop prods.
PT   for use in detection, diagnosis, vaccines and therapy of
PT   hepatitis E virus infection
XX
PS   Example 1; Page 40; 114pp; English.
XX
CC   The sequences given in AAQ45198-200 and AAQ61687-777 are primers which
CC   were used in the isolation and amplification of the genomic sequence
CC   of the hepatitis E virus (HEV) strain SAR-55.  These primers were
CC   based on sequences derived from the SAR-55 strain and a strain from
CC   Burma (BUR-121).  The amplified sequence contains three open reading
CC   frames (ORFs).  The proteins encoded by this sequence can be used to
CC   stimulate the production of protective antibodies upon injection into
CC   a mammal that would serve to protect the mammal upon challenge with
CC   wild type HEV.  The proteins can be used for detection and diagnosis
CC   of HEV infection.  This cDNA was isolated from primates innoculated
CC   with stool suspensions obtained from hepatitis E patients.
XX
SQ   Sequence 29 BP; 6 A; 10 C; 9 G; 4 T; 0 other;

  Query Match             59.1%;  Score 13.6;  DB 15;  Length 29;
  Best Local Similarity   80.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 ATCGGCTCCGAGGCGGGAAA 22
           ||| ||||| |||||  |||
Db       8 ATCCGCTCCCAGGCGTCAAA 27


RESULT 15
AAT27471
ID   AAT27471 standard; DNA; 29 BP.
XX
AC   AAT27471;
XX
DT   27-NOV-1996  (first entry)
XX
DE   HEV strain Burma-121 derived reverse primer 81 (ORF-1).
```

XX
KW Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
KW structural region; antigen; detection; antibody; vaccine;
KW immunisation; infection; primer; Burma-121;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN WO9610580-A2.
XX
PD 11-APR-1996.
XX
PF 03-OCT-1995; 95WO-US13102.
XX
PR 03-OCT-1994; 94US-0316765.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Emerson SU, Purcell RH, Tsarev SA;
XX
DR WPI; 1996-209320/21.
XX
PT Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
PT antigenic protein useful in diagnosis, prophylaxis and treatment of
PT hepatitis E virus infection
XX
PS Example 1; Page 43; 121pp; English.
XX
CC The present sequence is a hepatitis E virus (HEV) strain Burma-121
CC derived primer, used in the isolation of the HEV strain SAR-55
CC cDNA. The HEV strain SAR-55 was implicated in an enterically
CC transmitted non-A, non-B hepatitis in Pakistan. The protein encoded
CC by the structural region of the virus (i.e. ORF-2), which is
CC capable of forming HEV like particles, is useful for the detection
CC of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera,
CC cerebrospinal fluid, tissue, urine or pleural fluid. The protein,
CC and anti-HEV antibodies generated using the protein, can also be
CC used in vaccines for immunising an animal against HEV infection.
CC The protein is identified as a band of greater than 50 kD
CC following SDS-PAGE of cell lysates of insect cells infected with
CC a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
CC expression vectors pPIC9-1779, -1780 and -1781.
XX
SQ Sequence 29 BP; 6 A; 10 C; 9 G; 4 T; 0 other;

Query Match 59.1%; Score 13.6; DB 17; Length 29;
Best Local Similarity 80.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       3 ATCGGCTCCGAGGCGGGAAA 22
           ||| ||||| |||||  |||
Db       8 ATCCGCTCCCAGGCGTCAAA 27
```

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